

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 22, 2003, 01:28:08 / Search time 3471 Seconds  
10253.925 Million cell updates/sec

Title: US-09-831-142b-1

Perfect score: 870

Sequence: 1 gaatttcgcagctgcggaa.....aaaaaataaaactcgag 870

Scoring table: IDENTITY NUC  
Gap: 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

GenBank:

1: gb.hgs.\*

2: gb.hgs.\*

3: gb.in.\*

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39: gb.in.\*

40: gb.in.\*

41: gb.in.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	870	100.0	870	6	AX024884 Sequence
2	850	97.7	850	3	PDA131051 Phol
3	834.8	96.0	834.8	3	PDA131053 Phol
4	834.8	96.0	834.8	3	PDA131054 Phol
5	818.8	91.0	818.8	3	PDA131054 Phol
6	799.2	91.9	818.8	3	PDA131054 Phol
7	797.2	91.6	802	3	PDA131052 Phol
8	685.4	78.8	1695	3	AF497971 Phol
9	685.4	78.8	1695	3	AF497971 Phol
10	51.8	6.0	49280	6	AX144567 Mus muscu
11	51.6	5.9	7218	6	166494 Sequence 14
12	48.2	5.5	272698	3	PLAALP4
13	47.4	5.4	9810	6	AX145329 Sequence
14	46.8	5.4	9810	6	AX145329 Sequence
15	46.8	5.4	1716	3	AX050867
16	46.4	5.3	659	9	EC022405 Homo sapi
17	46.4	5.3	853	3	AX119449 broscapil
18	46.2	5.3	5443	3	AX150095 dictyoste
19	46.2	5.3	5443	3	AX150095 dictyoste
20	46.2	5.3	236824	2	AC097485
21	46	5.3	151802	3	AC114263 dictyoste
22	46	5.3	179938	2	AC1141012
23	45.8	5.3	12955	10	BC021442 Mus muscu
24	45.8	5.3	12955	10	BC021442 Mus muscu
25	45.8	5.3	12955	10	BC021442 Mus muscu
26	45.8	5.3	205281	2	AC139217 Mus muscu
27	45.8	5.3	219204	2	AC110090 Mus muscu
28	45.8	5.3	219204	2	AC110090 Mus muscu
29	45.6	5.2	283078	6	HS0801560
30	45.4	5.2	546	10	BC026533 Mus muscu
31	45.4	5.2	1257	9	BC043535 Homo sapi
32	45.4	5.2	1504	9	BC044260 Homo sapi
33	45.4	5.2	1504	9	BC044260 Homo sapi
34	45.4	5.2	2091	17	AB070046 Maccaca fa
35	45.4	5.2	2158	9	AB070046 Maccaca fa
36	45.4	5.2	136240	3	AC117070 dictyoste
37	45.4	5.2	178733	2	AC005308 Plasmodiu
38	45.4	5.2	178733	2	AC005308 Plasmodiu
39	45.4	5.2	267250	2	AC098041 Rattus no
40	45.4	5.2	303091	2	AC084799 Mus muscu
41	45.4	5.2	349880	6	AX144553 Sequence
42	45.4	5.2	349880	6	AX144553 Sequence
43	45.2	5.2	110000	2	PF041330
44	45.2	5.2	110000	2	PF041330
45	45.2	5.2	182871	3	AC117176 dictyoste

## ALIGNMENTS

RESULTS	Sequence	870 bp	DNA	linear	PAT 15-SEP-2000
AX024884	Sequence 1 from Patent WO0280255.				
AX024884	Sequence 1 from Patent WO0280255.				
AX024884.1	GI:10184825				
Pholas dactylus					
Pholas dactylus					
Pholadidae; Pholadidae; Pholas.					
Eukaryote; Metazoa; Mollusca; Bivalvia; Heterocomchia; Veneroide;					
Campbell A.K.					
Pholasin					
Patent: WO 028025-A 1 18-MAY-2000;					

Pred. No. is the number of results predicted by chance to have a

bad data

UNIV WALES MEDICINE (GB) ; CAMPBELL ANTHONY KEITH (GB)

FEATURES

Location/Qualifiers

source

BASE COUNT 289 a 153 c 213 g 205 t

ORIGIN

Query Match 100.0%; Score 870; DB 6; Length 870;

Best Local Similarity 100.0%; Pred. No. 1.9e-208;

Matches 870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCGACGACGTCGGAAAGACAAATGGCTGATGCTTGCTGCTGTCG 60

DB 1 GATTCGACGACGTCGGAAAGACAAATGGCTGATGCTTGCTGCTGTCG 60

QY 61 CTGATGCTGCTTAATCAGACGGGTCGGGTGAGGACGATGCGATGAATGACAC 120

DB 61 CTGATGCTGCTTAATCAGACGGGTCGGGTGAGGACGATGCGATGAATGACAC 120

QY 61 CTGATGCTGCTTAATCAGACGGGTCGGGTGAGGACGATGCGATGAATGACAC 120

DB 61 CTGATGCTGCTTAATCAGACGGGTCGGGTGAGGACGATGCGATGAATGACAC 120

QY 121 AAGCTTAATGAATGATGATGATGATGATGATGATGATGATGATGATGATG 180

DB 121 AAGCTTAATGAATGATGATGATGATGATGATGATGATGATGATGATGATG 180

QY 121 AAGCTTAATGAATGATGATGATGATGATGATGATGATGATGATGATGATG 180

DB 121 AAGCTTAATGAATGATGATGATGATGATGATGATGATGATGATGATGATG 180

QY 181 CTCATGACGACGATCTGATGATGATGATGATGATGATGATGATGATGATG 240

DB 181 CTCATGACGACGATCTGATGATGATGATGATGATGATGATGATGATGATG 240

QY 181 CTCATGACGACGATCTGATGATGATGATGATGATGATGATGATGATGATG 240

DB 181 CTCATGACGACGATCTGATGATGATGATGATGATGATGATGATGATGATG 240

QY 241 CAGTACACCAAAAGCGGCTGATGATGATGATGATGATGATGATGATGATGATG 300

DB 241 CAGTACACCAAAAGCGGCTGATGATGATGATGATGATGATGATGATGATGATG 300

QY 301 GAAATGACGACGATCTGATGATGATGATGATGATGATGATGATGATGATG 360

DB 301 GAAATGACGACGATCTGATGATGATGATGATGATGATGATGATGATGATG 360

QY 301 GAAATGACGACGATCTGATGATGATGATGATGATGATGATGATGATGATG 360

DB 301 GAAATGACGACGATCTGATGATGATGATGATGATGATGATGATGATGATG 360

QY 361 AGGACGACGACGATCTGATGATGATGATGATGATGATGATGATGATGATG 420

DB 361 AGGACGACGACGATCTGATGATGATGATGATGATGATGATGATGATGATG 420

QY 421 AGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480

DB 421 AGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480

QY 481 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540

DB 481 TTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540

QY 541 GTAGTGTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 600

DB 541 GTAGTGTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 600

QY 541 GTAGTGTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 600

DB 541 GTAGTGTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 600

QY 601 AGATGTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 660

DB 601 AGATGTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 660

QY 661 ACAGCTGTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 720

DB 661 ACAGCTGTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 720

QY 721 CTTTATGACGAGGACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780

DB 721 CTTTATGACGAGGACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780

QY 781 GTTAAATGACGAGGACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840

DB 781 GTTAAATGACGAGGACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840

QY 841 AATATGACGAGGACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 870

DB 841 AATATGACGAGGACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 870

RESULTS

Location/Qualifiers

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

QY 15 TCGAAGACGACAAATGGCTGATGCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 74

DB 1 TCGAAGACGACAAATGGCTGATGCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 74

QY 75 CAGACGGGTCGGGTGAGGACGATGATGCGATGAATGACGACGATGATGATGATG 134

DB 75 CAGACGGGTCGGGTGAGGACGATGATGCGATGAATGACGACGATGATGATGATG 134

QY 61 CAGACGGGTCGGGTGAGGACGATGATGCGATGAATGACGACGATGATGATGATG 120

DB 61 CAGACGGGTCGGGTGAGGACGATGATGCGATGAATGACGACGATGATGATGATG 120

QY 135 GTTTCATGACGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 194

DB 135 GTTTCATGACGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 194

QY 121 GTTTCATGACGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 180

DB 121 GTTTCATGACGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 180

PDAL1051

Pholas dactylus mRNA for pholasin.

Accession AJ131051

GI:4454298

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PDAL1051

Pholas dactylus mRNA for pholasin.

Accession AJ131051

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[illegible]















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PAGE COUNT      566 a      119 c      221 g      810 t
ORIGIN

Query Match      5.4%; Score 46.8; DB 3; Length 1716;
Best Local Similarity 58.7%; Pred. No. 0.58; Indels 0; Gaps 0;
Matches 81; Conservative 0; Mismatches 57;

OY 729 AGCAGGACACTGGTTCACGACACTATAACGTCCTCATCAATGAGGTGAAA 788
DB 150 ATCAAGTAATAGTCAATACCACTCTTCACGATTTAAGAAATATTCCTCACTCAA 91
OY 789 CAGAAATAATCGATAGATATCGAATATAATGTTAATACACCTGGTTCGAATATGAA 848
DB 90 AAAAAATCTAATTTTTTATATATAAAAAAATATAAAAAAAATTTATTATACATAA 31
OY 843 AAAAAAATAAAAAAACT 866
DB 30 AAAAAAATAAAAAAACT 13

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Search completed: August 22, 2003, 05:52:56  
 Job time : 3478 secs

Result No.	Score	Query Match	Length	DB	ID	Description	
1	870	100.0	870	21	AAAI5211	cDNA sequence from	
2	834.8	96.0	832.1	21	AAAI5211	PCR amplified geno	
3	795.2	94.0	818	21	AAAI5211	PCR amplified geno	
4	786.2	93.0	818	21	AAAI5211	PCR amplified geno	
5	772.5	83.3	776.1	21	AAAI5215	Human immune syste	
c	6	47.4	5	9610	4	AB132427	Human immune syste
7	47.4	5.4	47.4	4	AB132427	Human immune syste	
8	47.4	5.4	47.4	758	24	AEV83932	Human polynucleoti

C	9	46.2	5.3	9741	21	ABV53323	
10	45.6	5.2	360	23	ABV59054		
11	45.6	5.2	3028	24	ABV93725		
12	45.6	5.2	3028	24	ABV93725		
13	45.6	5.2	2691	24	ABV59022		
14	45.4	5.2	2710	21	ABV54132		
15	45.5	5.2	17294	24	ABV53287		
16	44.8	-5.1	6211	24	ABV52806		
17	44.8	-5.1	6211	24	ABV52806		
18	44.8	-5.1	6401	24	ABV52806		
19	43.8	5.0	363	25	ABV65522		
20	43.8	5.0	929	24	ABV64553		
21	43.4	5.0	11745	24	ABV84832		
22	43.4	5.0	11745	24	ABV84832		
23	43.4	5.0	131	25	ACV5065		
24	43.2	5.0	131	25	ACV5065		
25	43.2	5.0	131	25	ACV50674		
26	43.2	5.0	1321	24	ABV98825		
27	43.2	5.0	2185	24	ABV45822		
28	43.2	5.0	2185	24	ABV45822		
29	43.2	5.0	5643	24	ABV54638		
30	43.2	5.0	5649	24	ABV40008		
31	43.2	5.0	5649	24	ABV43284		
32	43.2	4.9	1501	24	ABV51008		
33	43.2	4.9	1501	24	ABV51008		
34	43.2	4.9	1904	25	ACV3652		
35	43.2	4.9	1904	25	ACV40473		
36	43.2	4.9	1904	25	ACV9150		
37	43.2	4.9	6235	24	ABV8202		
38	43.2	4.9	6235	24	ABV8202		
39	42.8	4.9	203	24	ABV33631		
40	42.8	4.9	203	24	ABV18446		
41	42.8	4.9	276	25	ABV44966		
42	42.8	4.9	524	25	ABV22885		
43	42.8	4.9	526	22	ABV72823		
44	42.8	4.9	935	21	ABV95101		
45	42.8	4.9	1655	25	ABV12483		

ALIGNMENTS

RESULT 1

AAV15211

ID AAV15211 standard; cDNA; 870 BP.

XX AAV15211;

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## ALIGNMENTS

RESULT 1  
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ID AAA15211 standard: cDNA: 870 BP.

DT 04-SEP-2000 (first entry)

**DE** cDNA sequence from clone 40 encoding apopholasin.

2421  
KW Bivalve mollusc; apopholasin; bioluminescent oxidative indicator protein;  
KW BOIP; light emission; pholasin; oxygen; chemiluminesce; cancer cell;  
KW hvocactive cell; rheumatoid arthritis; inflammatory disease: ss.

XX pholas dactylus.

AA	Key	Location/Qualifiers
EE		

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FT      CDS
FT      30..70/
FT      /*tag= a
FT      /product= "apomorphine"

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XX PN W0200028025-A1

18-MAY-2000

05-NOV-1999.

XX  
07-NOV-1998. 08GB-0024357

DA 10044-1 UNIV SERIES COLLEGE OF MEDICINE

PI Campbell AK:  
 XX WPI: 2000-387420/33.  
 XX P-PSUB: AN93251.  
 CC Novel recombinant nucleic acid molecules that encode the apophospholipase  
 CC of pholasin or its homologous sequence useful for detecting location  
 CC and measurement of oxygen and its metabolites in living cells and  
 CC organs.  
 XX Claim 3; Fig 1; 49pp; English.  
 XX The present sequence encodes a bivalve mollusc apophospholipase protein.  
 CC The protein is a bioluminescent oxidative indicator protein (BOIP).  
 CC Changes in light emission of pholasin enable oxygen or its metabolites  
 CC to be detected and quantified in live cells, organelles or on the outer  
 CC surface of cells. The protein is useful as a tool for measuring oxygen  
 CC in an organism without the need to break them open or the need to separate  
 CC bound and free fractions. This also enables an enzyme producing oxygen  
 CC or one of its metabolites to be detected and quantified. The BOIP is  
 CC metabolites intracellularly or extracellularly. The BOIP includes a  
 CC signal peptide whose target is set to a predetermined extra or  
 CC intracellular site. The light emission preferably takes place in the  
 CC absence of the phospholipase. The protein is also useful as a tool for  
 CC measuring oxygen in an organism without the need to break them open or  
 CC such as beer, cola, soft drinks and spirits to make them glow since  
 CC pholasin is able to chemiluminesce at a wide range of pH (3-10). It can  
 CC also be added to foodstuffs and in a wide range of toys and other  
 CC products. The protein is also useful as a tool for measuring oxygen and  
 CC location of abnormal cells such as cancer cells, hyperactive cells in  
 CC rheumatoid arthritis and other inflammatory diseases, cells infected with  
 CC a pathogen, damaged cells, and measurement and location of enzymes.  
 XX Sequence 870 BP; 289 A; 163 C; 213 G; 205 T; 0 other;  
 XX Query Match 100.0%; Score 870; DB 21; Length 870;  
 XX Best Local similarity 100.0%; Pred. No. 1.1e-206;  
 XX Matches 870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAATTCGACAGCTCGGAGAGAGAAATGGCTGTATGCTTCTCTCTGTC 60  
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 QY 61 CTCTATCTTATACAGCTGCTGCTGAGAGATGATATCCGAGATGAGAC 120  
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 DB 121 AGCTATGATATGCTGCTGAGCTGAGTACCTATTCATACAGATGAGGC 180  
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 DB 181 CTGAGAGCACTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
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 QY 301 GAG 360  
 DB 301 GAG 360  
 QY 361 AG 420  
 DB 361 AG 420  
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 DB 421 ACATCTTATGAGCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAG 480  
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DB 481 TTGTGCTGAGCTGAGGCTGCTCTATATACAGAGAGATGATGCTGATG 540  
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 QY 601 AGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660  
 DB 601 AGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660  
 QY 661 AGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720  
 DB 661 AGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720  
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 QY 781 AGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840  
 DB 781 AGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840  
 QY 841 AGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 870  
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 XX RESULT 2  
 XX ID AN93251  
 XX ID AN93251 standard; cDNA; 852 BP.  
 XX AC AAA15213;  
 XX DX 04-SEP-2000 (first entry)  
 XX DE cDNA sequence from clone 5 encoding apophospholipase.  
 XX KW Bivalve mollusc; apophospholipase; bioluminescent oxidative indicator protein;  
 XX KW BOIP; light emission; pholasin; oxygen; chemiluminescence; cancer cell;  
 XX KW hyperactive cell; rheumatoid arthritis; inflammatory disease; ss.  
 XX XX Pholas dactylus.  
 XX FH Key Location/Qualifiers  
 XX FT CDS 17..694  
 XX FT /\*tag= a  
 XX FT /product= "apophospholipase"  
 XX FN W0200028025-AL.  
 XX DB 18-MAY-2000.  
 XX DP 05-NOV-1999; 99NO-GB03654.  
 XX FR 07-NOV-1998; 98GB-0043357.  
 XX PR (UWVA-) UNIV WALES COLLEGE OF MEDICINE.  
 XX XX Campbell AK;  
 XX XX WPI: 2000-387420/33.  
 XX XX P-PSUB: AN93251.  
 XX Novel recombinant nucleic acid molecules that encode the apophospholipase  
 XX of pholasin or its homologous sequence useful for detecting location  
 XX and measurement of oxygen and its metabolites in living cells and  
 XX organs.  
 XX Claim 3; Fig 1; 49pp; English.  
 XX The present sequence encodes a bivalve mollusc apophospholipase protein.  
 XX The protein is a bioluminescent oxidative indicator protein (BOIP).

[illegible]

QY	734	GACACCTGGTGGTACAGACACCTATACGGTGTCTCTCATATATGTGTAAACAGAA	739
DB	735	AT	740
DB	721	GACACCTGGTGGTACAGACACCTATACGGTGTCTCTCATATATGTGTAAACAGAA	780
QY	794	AT	853
DB	781	AT	840
QY	851	AAAAAA 859	
QY	841	AAAAAA 846	
RESULT 3			
AAAL5214			
ID	AAAL5214 standard; cDNA; 818 BP.		
XX	AAAL5214;		
XX	AAAL5214;		
DT	04-SEP-2000 (first entry)		
PCR amplified genomic sequence of apopholasin DNA.			
DE	Bivalve mollusc; apopholasin; bioluminescent oxidative indicator protein;		
DE	BOIP; light emission; pholasin; oxygen; chemiluminescence; cancer cell;		
KW	hypertic cell; rheumatoid arthritis; inflammatory disease; ss.		
XX	Pholasin acetylus.		
XX	W0200028025-A1.		
PN	18-MAY-2000.		
XX	18-MAY-2000.		
PF	05-NOV-1999; 99NC-G803654.		
PR	07-NOV-1999; 98GB-0024357.		
PA	(UWVA) UNIV WALES COLLEGE OF MEDICINE.		
PI	Campbell AK;		
PI	WPI; 2000-387420/33.		
PT	Novel recombinant nucleic acid molecules that encode the apopholprotein		
PT	of pholasin or its homologous sequence useful for detecting location		
PT	and measurement of oxygen and its metabolites in living cells and		
PT	organs.		
PS	Disclosure: Fig 6; 49pp; English.		
XX	The present sequence represents a PCR amplified genomic sequence of		
XX	apopholasin DNA. The protein is a bioluminescent oxidative indicator		
CC	protein (BOIP). Changes in light emission of pholasin enable oxygen or		
CC	its metabolites to be detected and quantified in live cells, organelles		
CC	on the outer or inner surface of the plasma membrane, or within an		
CC	to separate bound and free fractions. This also enables an enzyme		
CC	producing oxygen or one of its metabolites to be detected and quantified.		
CC	The BOIP is used for the detection, diagnosis or measurement of oxygen or		
CC	its metabolites intracellularly or extracellularly. The BOIP includes a		
CC	intracellular site. The light emission preferably takes place in the		
CC	absence of the luciferase. Pholasin is also useful as a protein or a DNA		
CC	label or in genetic entertainment which involves adding pholasin to drink		
CC	such as beer, cola, soft drinks and spirits to make them glow, since		
CC	also be added to foodstuffs and in a wide range of toys and other		
CC	entertaining devices. BOIP nucleic acids can be used for detection and		
CC	location of abnormal cells such as cancer cells, hypertensive cells in		
CC	rheumatoid arthritis and other inflammatory diseases, cells infected with		
CC	a pathogen, damaged cells, and measurement and location of enzymes.		









PR	14-AUG-2000;	2000US-225758P.	PR	08-NOV-2000;	2000US-246610P.
PR	14-AUG-2000;	2000US-225759P.	PR	08-NOV-2000;	2000US-246611P.
PR	18-AUG-2000;	2000US-226279P.	PR	08-NOV-2000;	2000US-246613P.
PR	22-AUG-2000;	2000US-226568P.	PR	17-NOV-2000;	2000US-249207P.
PR	22-AUG-2000;	2000US-226569P.	PR	17-NOV-2000;	2000US-249208P.
PR	23-AUG-2000;	2000US-227182P.	PR	17-NOV-2000;	2000US-249209P.
PR	23-AUG-2000;	2000US-227009P.	PR	17-NOV-2000;	2000US-249210P.
PR	01-AUG-2000;	2000US-228241P.	PR	17-NOV-2000;	2000US-249211P.
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PR	08-SEP-2000;	2000US-231414P.	PR	17-NOV-2000;	2000US-249227P.
PR	08-SEP-2000;	2000US-232080P.	PR	17-NOV-2000;	2000US-249228P.
PR	12-SEP-2000;	2000US-232081P.	PR	17-NOV-2000;	2000US-249229P.
PR	14-SEP-2000;	2000US-232397P.	PR	17-NOV-2000;	2000US-249230P.
PR	14-SEP-2000;	2000US-232398P.	PR	01-DEC-2000;	2000US-250160P.
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PR	14-SEP-2000;	2000US-232400P.	PR	05-DEC-2000;	2000US-250162P.
PR	14-SEP-2000;	2000US-232401P.	PR	05-DEC-2000;	2000US-250163P.
PR	14-SEP-2000;	2000US-232603P.	PR	05-DEC-2000;	2000US-251030P.
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PR	21-SEP-2000;	2000US-234271P.	PR	08-DEC-2000;	2000US-251185P.
PR	21-SEP-2000;	2000US-234272P.	PR	08-DEC-2000;	2000US-251186P.
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PR	29-SEP-2000;	2000US-236370P.	PR	08-DEC-2000;	2000US-251196P.
PR	02-OCT-2000;	2000US-236802P.	PR	08-DEC-2000;	2000US-251197P.
PR	02-OCT-2000;	2000US-237037P.	PR	08-DEC-2000;	2000US-251198P.
PR	02-OCT-2000;	2000US-237038P.	PR	08-DEC-2000;	2000US-251199P.
PR	02-OCT-2000;	2000US-237039P.	PR	08-DEC-2000;	2000US-251200P.
PR	02-OCT-2000;	2000US-237040P.	PR	08-DEC-2000;	2000US-251201P.
PR	13-OCT-2000;	2000US-239933P.	PR	08-DEC-2000;	2000US-251202P.
PR	13-OCT-2000;	2000US-239937P.	PR	08-DEC-2000;	2000US-251203P.
PR	13-OCT-20				





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PR 17-FEB-2000; 2000US-183131P.
PR 16-MAR-2000; 2000US-189662P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-213045P.
PR 08-JUN-2000; 2000US-213046P.
PR 13-DEC-2000; 2000US-255281P.
XX (MIL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PA Schlegel R, Endege WO, Monahan JE;
XX PR 2001-667795/76.
XX WI; 2001-667795/76.
XX PR Novel isolated nucleic acid molecule associated with cancerous state of
XX PR prostate cancer, comprising the nucleic acid molecule useful
XX PR for detecting presence of prostate cancer, stage of prostate cancer;
XX PR claim 1: Page 11/298; 11750pp; English.
XX PS The invention relates to an isolated nucleic acid molecule (I) comprising
XX PS a nucleotide sequence given in Tables 1-9 (AB700010-AB762213) of the
XX PS specification or its complement. (I) is useful for:
XX CC (a) assessing whether a patient is afflicted with prostate cancer;
XX CC (b) monitoring progression of prostate cancer;
XX CC (c) assessing the efficacy of a test compound to inhibit prostate
XX CC cancer in a patient;
XX CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
XX CC in a patient; a composition for inhibiting prostate cancer in a patient;
XX CC (e) assessing the prostate cell carcinogenic potential of a compound;
XX CC (f) determining whether prostate cancer has metastasized in a patient;
XX CC (g) assessing the aggressiveness or indolence of prostate cancer in a
XX CC patient;
XX CC (h) also useful as a pharmacodynamic or pharmacogenomic marker.
XX PS Sequence 488 BP; 229 A; 100 C; 67 G; 92 T; 0 other;
XX PS
XX PS Query Watch
XX PS Best Local Similarity 53.0%; Score 45.4; DP 23; Length 488;
XX PS Matches 97; Conservative 0; Mismatches 0; Gaps 0;
XX QY 682 CAGAACTGCGAATTCCTGCTGAGTCATCTACAGACATCTTTCACGAGSACAGCTG 741
XX DB 76 CAGAACTGACATCTCAATGTCGTCGTAAGTGTCTTACTCTACTCTGAGTATAC 135
XX QY 743 TGTCTTCACGACGACATCTATCGTCTCTCATCATATGATGTAAGACGAAATATCGA 801
XX DB 132 TCTCTTCATGCTCTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 164
XX QY 802 TGAAGATCTGAAATATAAATGTTTATATTAACGCTGGTGTGAATATGAAAAA 861
XX DB 196 AAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA 195
XX QY 862 AAA 864
XX DB 256 AAA 258
XX QY
XX DB
XX RESULT 13
XX AAL50827
XX ID AAL50827 standard; DNA, 2091 BP.
XX AC
XX AC AAL50827;
XX DT 30-JUN-2003 (first entry)
XX DT Human cancer status prediction method-related DNA sequence #19.
XX XX Human; gene therapy; cancer status prediction; cancer; ds;
XX KN cancer malignancy evaluation; drug design; antisense nucleic acid.
XX XX Homo sapiens.
XX XX

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Search completed: August 22, 2003, 04:54:50  
Job time : 302 secs



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	2	43	4.9	2665	4	US-08-971-089-5	Sequence 5, Appl	
	3	41.6	4.8	1872	4	US-09-801-052-1	Sequence 1, Appl	
	4	41.6	4.8	1872	4	US-09-801-052-1	Sequence 1, Appl	
	5	41.4	4.8	2246	4	US-09-083-589-3	Sequence 3, Appl	
	6	40.2	4.6	6671	1	US-08-280-443-1	Sequence 1, Appl	
	7	40.2	4.6	6671	1	US-08-280-443-1	Sequence 1, Appl	
	8	40.2	4.6	6671	1	US-08-457-459-1	Sequence 1, Appl	
	9	40.2	4.6	6671	1	US-08-457-459-1	Sequence 1, Appl	
	10	40	4.6	2671	6	US-09-052-0275-1	Sequence 1, Appl	
C	1	39.6	4.6	3275	4	US-09-370-938-151	Sequence 151, Appl	
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	3	39.6	4.6	2621	2	US-08-553-619-98	Sequence 98, Appl	
	4	39.4	4.5	903	5	US-08-553-619-98	Sequence 98, Appl	
	5	39.2	4.5	2184	3	US-08-553-619-98	Sequence 98, Appl	
	6	39.2	4.5	2184	3	US-08-553-619-98	Sequence 98, Appl	
	7	39.2	4.5	2184	3	US-08-553-619-98	Sequence 98, Appl	
	8	38.8	4.5	2852	3	US-09-027-137-2	Sequence 2, Appl	
	9	38.8	4.5	2852	4	US-09-344-441-2	Sequence 2, Appl	
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	3	38.6	4.4	1174	4	US-09-501-115-5	Sequence 5, Appl	
	4	38.6	4.4	1174	4	US-09-501-115-5	Sequence 5, Appl	
	5	38.6	4.4	3327	2	US-09-909-965C-7	Sequence 7, Appl	
	6	38.6	4.4	6152	4	US-08-973-462-1	Sequence 1, Appl	
	7	38.4	4.4	1284	4	US-09-797-909C-50	Sequence 50, Appl	
	8	38.4	4.4	1284	4	US-09-797-909C-50	Sequence 50, Appl	
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; STRANDEDNESS: single
; TOPOLOGY: linear
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US-09-081507-3
Query Match          4.8%; Score 41.4; DB 4; Length 2246;
Best Local Similarity 61.7%; Pred: No. 0.05;
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Oy      758 TTTATGCTGTCTCCACAAATGTCATAGTCAATGAAGAAGAACGGTGATGCGAATAA 617
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DB       2117 TTATAGTGTACTGCACAAAACAAAAAAAAAAAAAAAAAAAAAAAAAA 2176
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Oy      818 AATTGTATTATACACTGTTGAAATGTGAATAAAAAAAAAAAAAA 864
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DB       2177 AGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2223
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RESULT 6
; Sequence 1, Application US/0928043
; Sequence 2, Application US/0928043
; General Information.

```

TITLE OF INVENTION: RNA Editing Enzymes and Methods of Use  
 INVENTOR: ROBERT S. HANCOCK  
 ADDRESS: Rowson and Rowson  
 CORRESPONDENCE ADDRESS:  
 SPRING HOUSE CORPORATE CTR., P.O. BOX 457  
 SPRING HOUSE, PENNSYLVANIA  
 COUNTRY: USA  
 COMPUTER-READABLE FORM:

[illegible]

QY 832 ACTGTTGAAATGAGAAAAAAGAAAAA 864  
 Db 6621 AAAAAAAGAAAAAAGAAAAAAGAAAA 6653

## RESULT 7

US-08-457-459-1  
 ; Sequence 1, Application US/08457459  
 ; Patent No. 567426  
 ; INVENTOR: Nishikura, Kazuko  
 ; APPLICANT: Nishikura, Kazuko  
 ; TITLE OF INVENTION: RNA Editing Enzyme and Methods of Use  
 ; NUMBER OF SEQUENCES: 39  
 ; NUMBER OF INVENTIONS: 1  
 ; CORRESPONDENT ADDRESS:  
 ; ADDRESS: Spring House Corporate Cntr, P.O. Box 457  
 ; CITY: Spring House  
 ; STATE: Pennsylvania  
 ; COUNTRY: USA  
 ; ZIP: 19477  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; MEDIUM: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/457,459  
 ; FILING DATE: 25-JUL-1994  
 ; PRIORITY DATA:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/197,794  
 ; FILING DATE: 17-FEB-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/280,443  
 ; FILING DATE: 25-JUL-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; REFERENCE/DOCKET NUMBER: N9149CUSA  
 ; TELEPHONE: 215-540-9206  
 ; TELEFAX: 215-540-9206  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 6671 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: cDNA  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 155..3822  
 ; US-08-457-459-1

Query Match 4.6%; Score 40.2; DB 1; Length 6671;  
 Best Local Similarity 64.5%; Pred. No. 0.18; 33; Indels 0; Gaps 0;  
 Matches 60; Conservative 0; Mismatches 33;

QY 772 ATCAATATGTTGAAGAAATATCGATAGAAATATGAAATATTTATTAAC 831  
 Db 6561 AACAGAAATCTGAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 6620  
 QY 832 ACTGTTGAAATGAGAAAAAAGAAAAA 864  
 Db 6621 AAAAAAAGAAAAAAGAAAAAAGAAAAA 6653

## RESULT 8

US-08-555-678-1  
 ; Sequence 1, Application US/0855678  
 ; Patent No. 5763174

GENERAL INFORMATION  
 ; TITLE OF INVENTION: RNA Editing Enzyme and Methods  
 ; TITLE OF INVENTION: RNA Editing Enzyme and Methods  
 ; NUMBER OF SEQUENCES: 67  
 ; NUMBER OF INVENTIONS: 1  
 ; CORRESPONDENT ADDRESS:  
 ; ADDRESS: Spring House Corporate Cntr, P.O. Box 457  
 ; CITY: Spring House  
 ; STATE: Pennsylvania  
 ; COUNTRY: USA  
 ; ZIP: 19477  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; MEDIUM: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/555,678  
 ; FILING DATE: 25-JUL-1994  
 ; PRIORITY DATA:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/197,794  
 ; FILING DATE: 17-FEB-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/280,443  
 ; FILING DATE: 25-JUL-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; REFERENCE/DOCKET NUMBER: N9149CUSA  
 ; TELEPHONE: 215-540-9206  
 ; TELEFAX: 215-540-9206  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 6671 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: cDNA  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 155..3822  
 ; US-08-555-678-1

Query Match 4.5%; Score 40.2; DB 1; Length 6671;  
 Best Local Similarity 64.5%; Pred. No. 0.18;  
 Matches 60; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 772 ATCAATATGTTGAAGAAATATCGATAGAAATATGAAATATTTATTAAC 831  
 Db 6561 AACAGAAATCTGAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 6620  
 QY 832 ACTGTTGAAATGAGAAAAAAGAAAAA 864  
 Db 6621 AAAAAAAGAAAAAAGAAAAAAGAAAAA 6653

## RESULT 9

PC-US95-02275-1  
 ; Sequence 1, Application PC/US9502275  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wistar Institute of Anatomy & Biology  
 ; TITLE OF INVENTION: RNA Editing Enzyme and Methods of Use  
 ; NUMBER OF SEQUENCES: 39  
 ; CORRESPONDENT ADDRESS:  
 ; ADDRESS: Spring House Corporate Cntr, P.O. Box 457  
 ; STREET: Spring House Corporate Cntr, P.O. Box 457

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; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; COUNTRY: 0417
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MS-DOS
; RELEASE DATE: 1998-08-06
; CURRENT APPLICATION DATA: Release #1.0, Version #1.30
; APPLICATION NUMBER: PCT/US95/02275
; FILING DATE:
; FILING DATE:
; FILING DATE:
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US 08/280,443
; FILING DATE: 25-JUL-1994
; PRIOR APPLICATION DATA: US 08/197,794
; FILING DATE: 17-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sak, Mary E. 31,215
; REFERENCE/DOCKET NUMBER: MST49BCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9206
; TELEFAX: 215-540-5818
; INTERNET:
; SEQUENCE CHARACTERISTICS: 1:
; LENGTH: 6671 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; ORIGIN: 135..3832
; PCT-US95-02275-1
;
Query Match
Best Local Similarity 64.6%; Score 40.2; DB 5; Length 6671;
Matches 60; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
;
QY 772 ATCATGTTGTGTAACACAGAAATATCGATAGATATGAAATAAATGTTAATAAC 831
Db 6561 AACGAGATCTGAAAAAGAAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAAA 6620
;
QY 832 ACTCGTGAATATGAAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAA 864
Db 6621 AAAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAAA 6653
;
RESULT 10
; Parent No. 5168051
; TITLE OF INVENTION: RIK M.A.-CORDELL, DAVID V.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION NUMBER:
; APPLICATION NUMBER: US 08/907,989, 929
; SEQ ID NO:9: DATE: 04-AUG-1989
; LENGTH: 2671
;
5168051-9
; TYPE: DNA
; ORGANISM: Homo sapiens
; SEQ ID NO 9: 135..3832
; LENGTH: 2671
;
Query Match
Best Local Similarity 65.9%; Score 40; DB 6; Length 2671;
Matches 58; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
;
QY 777 TATGCTGTAACAGAAATATCGATAGATATGAAATAAATGTTAATAACATCG 836
Db 2573 TATGCTGTAACAGAAATATCGATAGATATGAAATAAATGTTAATAACATCG 836
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QY 837 TGAATATGAAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAAA 864

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Db 2653 AAAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAA 2650
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RESULT 11
; Sequence 151, Application US/09370838
; FILE REFERENCE: P201 NUMBER: US/09370838
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Roshon
; APPLICANT: Mohamath, Roshon
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF LUNG CANCER AND METHODS FOR THEIR USE
; TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 21021.475C1
; CURRENT FILING DATE: US 09/370,838
; CURRENT FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: US 09/285,323
; EARLIER FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 289
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 151: LS8Q FOR WINDOWS Version 3.0
; LENGTH: 3275
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-370-838-151
;
Query Match
Best Local Similarity 63.5%; Score 40; DB 4; Length 3275;
Matches 61; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
;
QY 775 ATAATGCTGTAACAGAAATATCGATAGATATGAAATAAATGTTAATAACACT 834
Db 3180 AAAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAA 3239
;
QY 835 GOTTGAATATGAAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAA 870
Db 3240 AAAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAA 3275
;
RESULT 12
; Sequence 38, Application US/09489947
; FILE REFERENCE: P201 NUMBER: US/09489947
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteolins
; TITLE OF INVENTION: 98 Human Secreted Proteolins
; FILE REFERENCE: P201 NUMBER: US/09489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER FILING DATE: 1998-07-29/094,457
; EARLIER FILING DATE: 1998-07-29/094,457
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; NUMBER OF SEQ ID NOS: 2.0
; SEQ ID NO 38: Martin Ver. 2.0
; LENGTH: 1048
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-489-847-38
;
Query Match
Best Local Similarity 47.1%; Score 39.6; DB 4; Length 1048;
Matches 57; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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	Matches	72: Conservative	0: Mismatches	54: Indels	0: Gaps
Oy	Oy	799	CTGGTCTACGACACATCTATACGCTGCTCTCTATCAATGAGGCGAAGCAAGAAAT	798	
Db	Db	890	CTTTTGGTCTACGACGTCATCATATCTCTTATGATGAGGCGAAGCAAGAAAT	949	
Oy	Oy	799	CGTCAATATTGGAATGAAAATATTTATGACGCTGGTGGAATATGAAAATGAAAA	858	
Db	Db	950	AAAAAATGAAAAATGAAAAATGAAAAATGAAAAATGAAAAATGAAAAATGAAAA	1009	
Oy	Oy	859	AAAAA 864		
Db	Db	1010	AAAAA 1015		

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1 RESULT 13
2
3 : US-08-553-6198-6
4 : Sequence 8, Application US/085536198
5 :
6 : PATENT NO. 5919705
7 : GENETIC NAME:
8 : APPLICANT: Dehaan, Petrus T.
9 : TITLE OF INVENTION: Virus Resistant Plants
10 : NUMBER OF SEQUENCES: 30
11 : CROSS REFERENCE AKAUS: 30
12 : CROSS REFERENCE AKAUS: 5919705artis Crop Protection
13 : STREET: 975 California Avenue
14 : CITY: Palo Alto
15 : STATE: CA
16 : COUNTRY: USA
17 : ZIP: 94304
18 :
19 : COMPUTER READABLE FORM:
20 : MEDIUM TYPE: Floppy disk
21 : COMPUTER: IBM PC compatible
22 : SOFTWARE: IBM PC DOS/MS-DOS
23 : SOFTWARE: Patinto Release #1.0, Version #1.25
24 : CURRENT APPLICATION DATA:
25 : APPLICATION NUMBER: US/08/553-6198
26 : FILING DATE: December 1, 1995
27 : AGENT:
28 : ATTORNEY/AGENT INFORMATION:
29 : NAME: Marcus Winer, Lynn
30 : REGISTRATION NUMBER: 34,869
31 : REFERENCE/DOCKET NUMBER: 137-1082/PCT
32 : TRADEMARK/REGISTRATION INFORMATION:
33 : TELEPHONE: 415/354-3580
34 : TELEFAX: 415/857-1125
35 : INFORMATION FOR SEQ ID NO: 8:
36 : SEQUENCE CHARACTERISTICS:
37 : LENGTH: 1000 base pairs
38 : TYPE: nucleic acid
39 : STRANDEDNESS: single
40 : TOPOLOGY: unknown
41 : ORIGINAL SOURCE:
42 : ORGANISM: Chlamydia
43 : Chlamydia tomato spotted wilt virus S RNA
44 :
45 : US-08-553-6198-8

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[illegible]

RESULT 14  
PCT-US95-06406A-21  
; Sequence 21, Application PC/TUS9506406A  
; GENERAL INFORMATION:

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1  APPLICANT: Janet D. Robichaw, Charles Kunsch
2  TITLE OF INVENTION: cDNA Clones Encoding Human G Protein
3  NUMBER OF SEQUENCES: 23
4  COMPUTER FILE ADDRESS:
5  ADDRESS:
6  STREET:
7  CITY:
8  STATE:
9  COUNTRY:
10 ZIP:
11
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
14 OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
15 SOFTWARE: WORDPERFECT 5.1
16 CURRENT APPLICATION DATA:
17 PUBLICATION DATE:
18 CLASSIFICATION:
19 APPLICATION NUMBER: PCT/US95/06406A
20 PRIORITY DATE:
21 PRIORITY APPLICATION NUMBER:
22 PRIORITY APPLICATION DATE:
23 PUBLICATION DATE:
24 PUBLICATION NUMBER:
25 NAME:
26 REGISTRATION NUMBER:
27 REFERENCE/DOCKET NUMBER:
28 TECHNICAL INFORMATION:
29 TELEPHONE:
30 TELEFAX:
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32 INFORMATION FOR SEQ ID NO: 21:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 795
35 TYPE: Nucleic Acid
36 STRANDEDNESS: Single
37 TOPOLOGY: Linear
38 ANTI-SENSE: No
39 PCT-CLASS: 21
40
41 Query Match 4.5%; Score 39.4; DB 5; Length 903;
42 Best Local Similarity 56.6%; Pred. No. 0.12;
43 Matches 73; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
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45 QY 736 CAGATCGGCTGTACCAACACTATTAAGCGTCTCATATATGTGTAAACAGAAAT 795
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47 QY 764 CTATCTGGAGGGTAAACCCATTGAGAGATTAAGTCATCGAGCTCTAAAAAAAAA 823
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49 QY 796 AATCTGAGATATGGAATTAAGTCTATTAACCTGGTGTGAATTTGAAAAAA 855
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51 DB 824 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 883
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53 QY 856 AAAAAAAAA 864
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55 DB 884 AAAAAAAAA 892
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MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARES: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,918C
PRIORITY NUMBER: 08/955,918
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/697,766
FILING DATE: 29-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: JAMES E. SMITH
REGISTRATION NUMBER: 56,207
REFERENCE/DOCKET NUMBER: MNI-007CPDV2CPA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517)227-7400
FAX: (517)227-7401
E-MAIL: JESMITH@MNI.COM
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2184 base pairs
TYPE: nucleic acid
SUBMITTER: single
TOPOLAG: linear
MOLECULE TYPE: cDNA
FEATURES:
ORF1: 1..1616
ORF2: 1617..1616
US-08-955-918C-1

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Query Match          4.5%; Score 39.2; DB 3; Length 2184;
Best Local Similarity 60.8%; Prd. No. 0.21;
Matches 62; Conservative 1; Mismatches 39; Indels 0; Gaps 0;
QY 763 CGTGTCTTCATCATGTCGTAACGCGAATATCGATGATATGAAATATATG 822
Db 2057 CGGTCTTCGCGGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG 2116
QY 823 TTATTAACACTGTTGAAATATGAAAAAAGAAAAAAGAAAAAAG 864
Db 2117 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG 2158

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Search completed: August 22, 2003, 06:32:51  
Job time : 75 secs

Result	No.	Score	Query	Match	Length	DB	ID	Description
C	1	47.4	5.4	9810	12	US-10-311-455-400		Sequence 400, App
C	2	47.2	5.4	3999	4	US-10-198-386-1795		Sequence 1795, App
C	3	47.2	5.4	3999	4	US-10-198-386-1795		Sequence 1795, App
C	4	46.2	5.3	9741	12	US-10-311-455-1296		Sequence 1296, App
C	5	45	5.2	1794	12	US-10-311-455-960		Sequence 960, App
C	6	44.8	5.1	805	13	US-10-027-632-25968		Sequence 2596, App
C	7	44.8	5.1	805	13	US-10-027-632-25968		Sequence 2596, App
C	8	44.8	5.1	805	13	US-10-027-632-25968		Sequence 2596, App
C	9	44	5.1	6040	12	US-10-311-455-400		Sequence 400, App
C	10	43.8	5.0	363	10	US-09-960-321-1687		Sequence 1687, App
C	11	43.4	5.0	1145	12	US-10-240-453-206		Sequence 206, App
C	12	43.2	5.0	1113	11	US-09-938-959-7068		Sequence 7068, App
C	13	43.2	5.0	1113	11	US-09-938-959-7068		Sequence 7068, App
C	14	43.2	5.0	1321	11	US-09-926-299-235		Sequence 235, App
C	15	43.2	5.0	2852	10	US-09-761-640-2		Sequence 2, Appli
C	16	43.2	5.0	5649	12	US-10-311-455-822		Sequence 822, App



QY 714 CAGACACTTTCACGACGACACTGCTGTACACGACGACGACGACGCTGCTCTT 773  
 Db 3938 ACTATATATATCATCCCAATAAAGACAAATACTATCATCTCATATATTTTCATTC 3879  
 QY 774 CAGATATGTGAACAGAAATATATCATCATAGATATATGAATATATATATATATATATAC 833  
 Db 3878 CAAATATCTCTTAAGACAAACACTCTTCATCAACAAACAAACAAACAAATTTATATAT 3819  
 QY 834 TGGTGTGAATATGAAAAAAGAAAAAAGAAAAAAGCT 866  
 Db 3818 TTTTTCATATCAAT 3786  
 RESULT 2  
 US-10-198-846-12795/C  
 ; Sequence 1985, Application US/0198846  
 ; Publication No. US2003009974A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lilly, James  
 ; APPLICANT: Rosen et al.  
 ; APPLICANT: Wang, Wenzhen  
 ; APPLICANT: Steilmann, Kathleen  
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
 ; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
 ; FILE REFERENCE: US/049  
 ; CURRENT APPLICATION NUMBER: US/10/198,846  
 ; CURRENT FILING DATE: 2002-07-18  
 ; PRIOR APPLICATION NUMBER: 60/306,220  
 ; PRIOR FILING DATE: 2001-07-10  
 ; NUMBER OF SEQ ID NOS: 14084  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 12795  
 ; ORGANISM: Homo sapiens  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-198-846-12795

Query Match  
 Best Local Similarity 57.4%; Score 47.2; DB 14; Length 3999;  
 Matches 85; Conservative 0; Mismatches 63; Indels 0; Gaps 0;  
 QY 717 ACTCATTTTACGACGACGACGACGCTGTACGACGACGACGACGCTTACGCTCATCA 776  
 Db 183 ACTATGTAATGATGTATATACATCTTTTCATCATGATATATGATATGATCTGTCCA 124  
 QY 777 TATGTGTAT 836  
 Db 123 TTTAAGCATACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 64  
 QY 837 TGTAAATATGAAAAAAGAAAAAAGAAAAAAGAAAAA 864  
 Db 63 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 36

RESULT 3  
 US-10-764-853-161  
 ; Sequence 161, Application US/09764853  
 ; Publication No. US2002009067A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; APPLICANT: Tishler, Michael  
 ; FILE REFERENCE: P206  
 ; CURRENT APPLICATION NUMBER: US/09/764,853  
 ; CURRENT FILING DATE: 2001-01-17  
 ; PRIOR APPLICATION ORIGIN: removed - consult PAM or file wrapper  
 ; PRIOR APPLICATION NUMBER: 09/093,930  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 161  
 ; LENGTH: 758  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens

US-09-764-853-161  
 Query Match  
 Best Local Similarity 54.3%; Score 47; DB 9; Length 758;  
 Matches 95; Conservative 0; Mismatches 80; Indels 0; Gaps 0;  
 QY 690 GGGAGATCTTCTGTGTAT 749  
 Db 11 1111  
 QY 564 GAGAGCTGTATACAGGACACTCTGGGCCATGGTTTAAACCCAAATTAAGACGACAGAT 623  
 Db 754 CAGACGACATATACGCTGCTTCATCATATATATATATATATATATATATATATATATATAT 809  
 QY 624 ATGACACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 683  
 Db 810 TGAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 864  
 Db 684 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 738

RESULT 4  
 US-10-455-1296/C  
 ; Sequence 1296, Application US/0311455  
 ; Publication No. US2003014360A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Olek, Alexander  
 ; APPLICANT: Kurt, Christian  
 ; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by De  
 ; TITLE OF INVENTION: cytosine methylation  
 ; FILE REFERENCE: US/011455  
 ; CURRENT APPLICATION NUMBER: US/10/311,455  
 ; CURRENT FILING DATE: 2002-12-16  
 ; PRIOR APPLICATION NUMBER: EC/EPOL/07537  
 ; PRIOR FILING DATE: 2001-07-27; 10032529.7  
 ; PRIOR APPLICATION NUMBER: DE 10043826.1  
 ; PRIOR FILING DATE: 2000-06-30  
 ; PRIOR FILING DATE: 2000-09-01  
 ; NUMBER OF SEQ ID NOS: 2424  
 ; SOFTWARE: SeqScribe  
 ; SEQ ID NO 1296  
 ; LENGTH: 9741  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
 US-10-311-455-1296

Query Match  
 Best Local Similarity 62.3%; Score 46.2; DB 12; Length 9741;  
 Matches 69; Conservative 0; Mismatches 38; Indels 0; Gaps 0;  
 QY 758 TATATCTCTCTCATCAT 817  
 Db 6660 TATATCTCTCTCATCAT 5601  
 QY 818 AATGTGTAT 864  
 Db 6600 AAT 6554

RESULT 5  
 US-10-311-455-960/C  
 ; Sequence 960, Application US/0311455  
 ; Publication No. US2003014360A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Olek, Alexander  
 ; APPLICANT: Kurt, Christian  
 ; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by De  
 ; TITLE OF INVENTION: cytosine methylation  
 ; FILE REFERENCE: 5013.1014  
 ; CURRENT APPLICATION NUMBER: US/10/311,455  
 ; CURRENT FILING DATE: 2002-12-16



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? SEQ ID NO 11687
? LENGTH: 363
? TYPE: DNA
? ORGANISM: Bos taurus
? CLONING VECTOR: pUC19
? CLONE ID: 50-LIB3058-012-Q1-X1-E10
US-09-560-352-11687

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Best Local Similarity 56.6%; Pred. No. 0.18; Indels 0; Gaps 0;
Matches 81; Conservative 0; Mismatches 62

QY 722 TTTTACGCGAGGACACTGGCTGTTACACGACACTAAGCTGCTCATCAATATG 181
DB 171 TTTTCTCCCTTAATTCGCTGCTTTTCAACAGACGCCGCTTTTACTTTTACATTA 112
QY 762 TGTAAACAGATTAATGATGATATGAATTAATTAATGTAATTAACATGGTGA 841
DB 111 TATTAATTAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 52
QY 842 ATGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 864
DB 51 AAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 11
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? Sequence 206, Application US10240453
? Publication No. US20030148376A1
? PATENT NO.: 6,800,000
? APPLICANT: OLEY, Alexander
? APPLICANT: BERLIN, Kurt
? TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
? TITLE OF INVENTION: By Means of Assessing the Methylation Status of Genes Associ
? TITLE OF INVENTION: With DNA Transcription
? FILE REFERENCE: 5013-1009
? CURRENT FILING DATE: 2002-10-02
? PRIOR APPLICATION NUMBER: US/10/240,453
? PRIOR FILING DATE: 2001-04-06
? PRIOR APPLICATION NUMBER: DE 10019058.8
? PRIOR FILING DATE: 2000-04-07
? PRIOR APPLICATION NUMBER: DE 10019173.8
? PRIOR FILING DATE: 2000-04-07
? PRIOR APPLICATION NUMBER: DE 10032529.7
? PRIOR FILING DATE: 2000-04-06
? PRIOR APPLICATION NUMBER: DE 10034926.1
? PRIOR FILING DATE: 2000-09-01
? NUMBER OF SEQ IDS NOS: 350
? SEQ ID NO 206
? LENGTH: 11745
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
? NAME/SEQ: unsure
? LOCATION: (9105)
US-10-240-453-206

Query Match          5.0%; Score 43.4; DB 12; Length 11745;
Best Local Similarity 53.9%; Pred. No. 1.3;
Matches 89; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
QY 697 TGTCTGCGTGCATGCTGAGTCTTTTACACGACGACACTGGCTGCTACGACGAC 756
DB 6545 TATCTAATTAATCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 6490
QY 757 CTATACGCTGCTCTCATCAATATGTAATGTGTAACACGATTAATCATAGATATGAAT 816
DB 6489 CTAACAAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 9430

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Search completed: August 22, 2003, 06:43:51  
Job time : 652 secs



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724 TTATCAGCAGGACAACTGGTCGTTACAGACACCT





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mRNA sequence.
ACCESSION B125633
VERSION B125633.1 GI:15937183
KEYWORDS EST, sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLES (Cases 1 to 811)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rstraus@nih.gov
Phone: 301-495-4600
Fax: 301-495-4600
Address: National Institutes of Health, Bethesda, MD 20892
Tissue Procurement: Christopher A. Meskalluk, M.D., Ph.D., Michael
P. Haughey, M.D., Ph.D., Life Technologies, Inc.
DNA Library Prepared by: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: NIH-MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/NIH at:
http://image.llnl.gov
Plate: L14M11408 Row: 1 Column: 01
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/tissue_type="medulla"
/lab_host="DH108"
/clone_lib="NIH_MGC_119"
/notes="Organ: Brain; Vector: pCMV-Sport6; Site: 1; NotCl;
Note: This cDNA library was constructed from a total RNA
extracted from a 27 day embryonic mouse embryo. The library is
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
0.9-3 kb. Library is constructed by C. Lerger
(Invitrogen Research Specifics Tracking Code 015. Note:
this is a NIH-MGC Library."
BASE COUNT 319 a 182 c 163 g 147 t
Query Match 5.78; Score 49.4; DS 12; Length 811;
Best Local Similarity 58.3%; Pred. No. 5e+02;
Matches 86; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
QY 718 CTCTCTTTATCAGCAGCAGCAGCTGCTGTACAGCAGCTATACAGCTGTCTGTCAT 777
Db 119 CTCTCTTTATCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 178
QY 776 ATGCTGTAAACAGCAATATCGAGAGATATTCGAAATATTAATGTTATTAATACCTGGT 837
Db 175 ATGCTGTAAACAGCAATATTCGAGAGATATTCGAAATATTAATGTTATTAATACCTGGT 238
QY 838 TGAAATATGAAATATGAAATATGAAATATGAAATATGAAATATGAAATATGAAATATG 864
Db 239 AAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 265
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LOCUS B125633
DEFINITION B125633.1 Homo sapiens cDNA clone IMAGE:2291556 5',
mRNA sequence.
ACCESSION B125633
VERSION B125633.1 GI:8395113
KEYWORDS EST, sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLES (Cases 1 to 811)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rstraus@nih.gov
Phone: 301-495-4600
Fax: 301-495-4600
Address: National Institutes of Health, Bethesda, MD 20892
Tissue Procurement: Christopher A. Meskalluk, M.D., Ph.D., Michael
P. Haughey, M.D., Ph.D., Life Technologies, Inc.
DNA Library Prepared by: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: NIH-MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/NIH at:
http://image.llnl.gov
Plate: L14M11408 Row: 1 Column: 01
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LOCUS/Qualifiers
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/notes="Organ: Brain; Vector: pCMV-Sport6; Site: 1; Salt;
Note: This cDNA library was constructed from a total RNA
extracted from a 27 day embryonic mouse embryo. The library is
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.9 kb. Tumor
types include: meningioma, oligodendroglioma, astrocytoma
(Grade II), medulloblastoma, astrocytoma (Grade IV).
This project was funded by NIH grant NS39485."
BASE COUNT 210 a 25 c 58 g 92 t
Query Match 5.54; Score 48.2; DS 10; Length 385;
Best Local Similarity 51.6%; Pred. No. 1e+03;
Matches 110; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
QY 652 ACACGATGACGAGCTGAGACGACGCTGACGAGCTGAGCTGAGCTGAGCTGAGCTG 711
Db 105 ATGACAGCTGTGGCTATGAAAGAGGTTTTCGACGCTGCTATCTGATGATGGAGAT 164
QY 712 ATCAGACTCTTTATCAGCAGCAGCAGCTGCTGTACGACACTATACGCTGCTCCTC 771
Db 165 GACTTATTTTCTTTATGACGACGACGCTGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 224
QY 772 ATCAATATGCTGTAACCAAGAAATATTCGATAGAAATATGAAATATTAATATTAAC 831
Db 225 TTAATATTTTAAATTTTGAATATTAATATTAATATTAATATTAATATTAATATTAAC 284
QY 832 CTGCTGTGTAATATGAAATATGAAATATGAAATATGAAATATGAAATATGAAATATG 864
Db 285 AAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 317
RESULT 8
LOCUS A2196391/c
DEFINITION A2196391/c 752 bp DNA linear GSS 31-AUG-2000
SP_1031_92_G05_07A Strongylocentrotus purpuratus, purple sea urchin
clone plate-1031 Col-10 Row-A, genomic survey sequence.
ACCESSION A2196391
VERSION A2196391.1 GI:8390214
KEYWORDS GSS,
Strongylocentrotus purpuratus
Strongylocentrotus purpuratus
SOURCE Strongylocentrotus purpuratus
ORGANISM Eukaryota; Metazoa; Echinodermata; Echinozoa;
Echinoida; Euechinoidea; Echinoidea; Echinoidea; Echinoidea;

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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCI-MINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/Brain), Tumor Gene Index
Contact: Robert Strausberg, Ph.D.
Email: rstraus@nih.gov
Phone: 301-495-4600
Fax: 301-495-4600
Address: National Institutes of Health, Bethesda, MD 20892
Tissue Procurement: Christopher A. Meskalluk, M.D., Ph.D., Michael
P. Haughey, M.D., Ph.D., Life Technologies, Inc.
DNA Library Prepared by: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/NIH, send email to:
infocore@llnl.gov
Insert Length: 437 Std Error: 0.00
Seq Primer: -408P from gibco
High quality sequence stop: 369.
LOCUS/Qualifiers
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/mol_type="mRNA"
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/ab_xref="IMAGE:2291556"
/tissue_type="tumor, 5 pooled (see description)"
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/clone_lib="NIH_MGC_Brn52"
/notes="Organ: Brain; Vector: pCMV-Sport6; Site: 1; Salt;
Note: This cDNA library was constructed from a total RNA
extracted from a 27 day embryonic mouse embryo. The library is
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.9 kb. Tumor
types include: meningioma, oligodendroglioma, astrocytoma
(Grade II), medulloblastoma, astrocytoma (Grade IV).
This project was funded by NIH grant NS39485."
BASE COUNT 210 a 25 c 58 g 92 t
Query Match 5.54; Score 48.2; DS 10; Length 385;
Best Local Similarity 51.6%; Pred. No. 1e+03;
Matches 110; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
QY 652 ACACGATGACGAGCTGAGACGACGCTGACGAGCTGAGCTGAGCTGAGCTGAGCTG 711
Db 105 ATGACAGCTGTGGCTATGAAAGAGGTTTTCGACGCTGCTATCTGATGATGGAGAT 164
QY 712 ATCAGACTCTTTATCAGCAGCAGCAGCTGCTGTACGACACTATACGCTGCTCCTC 771
Db 165 GACTTATTTTCTTTATGACGACGACGCTGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 224
QY 772 ATCAATATGCTGTAACCAAGAAATATTCGATAGAAATATGAAATATTAATATTAAC 831
Db 225 TTAATATTTTAAATTTTGAATATTAATATTAATATTAATATTAATATTAATATTAAC 284
QY 832 CTGCTGTGTAATATGAAATATGAAATATGAAATATGAAATATGAAATATGAAATATG 864
Db 285 AAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 317
RESULT 8
LOCUS A2196391/c
DEFINITION A2196391/c 752 bp DNA linear GSS 31-AUG-2000
SP_1031_92_G05_07A Strongylocentrotus purpuratus, purple sea urchin
clone plate-1031 Col-10 Row-A, genomic survey sequence.
ACCESSION A2196391
VERSION A2196391.1 GI:8390214
KEYWORDS GSS,
Strongylocentrotus purpuratus
Strongylocentrotus purpuratus
SOURCE Strongylocentrotus purpuratus
ORGANISM Eukaryota; Metazoa; Echinodermata; Echinozoa;
Echinoida; Euechinoidea; Echinoidea; Echinoidea; Echinoidea;

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**TITLE**  
Unpublished  
**JOURNAL**  
**COMMENT**

The Washington Univ. Nematoe EST Project, 1999  
Contact: McCarter JP  
The Washington Univ. Nematoe EST Project, 1999  
Washington University School of Medicine  
660 South Euclid Avenue, Box 8304, St. Louis, MO 63109, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: jester@wustl.edu  
Web: <http://www.wustl.edu/est/>  
Image Consortium ([image.llnl.gov](http://image.llnl.gov)) contact the  
Image Consortium ([image.llnl.gov](http://image.llnl.gov)) for further information.  
High quality sequence stop: 339.

**FEATURES**  
source

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McCarter"  
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The library was constructed by Brandi Chiapelli and Dr.  
Anthony Wang on University of St. Louis. The  
cDNA was made by using double-stranded cDNA,  
PCR based library using a modified protocol from the  
SMART PCR cDNA Synthesis Kit from Clontech. Directionally  
cloned into the UDS sites of pAMP1."  
200 a 37 c 40 g 63 c

Query Match 5.5%; Score 47.6; DB 12: Length 346;  
Best Local Similarity 61.4%; Pred. No. 1.4e+03;  
Matches 77; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 740 TGGTGTGACAGACCTTAACTGCTCTCATCAATATGTAACAGAAATATC 799  
DB 150 TTTTCTTCATGAGACCTGTTCTGTCATGCAATATGATGATTCGAAAAA 209  
QY 800 GATGATATATGAATAAATGTTATTAACATGCTGTTCAATATGAATAAATAA 859  
DB 210 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 269  
QY 860 AAAAAA 865  
DB 270 AAAAAA 275

**RESULT 11**  
**LOCUS** BU566867  
**DEFINITION** AGNCOURT\_1039734; NIH\_MGC\_141 Homo sapiens cDNA clone  
**VERSION** BU566867  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

**REFERENCE**  
**AUTHORS** NIH-MGC http://mgc.ncl.nih.gov/  
**JOURNAL** National Institutes of Health, Mammalian Gene Collection (MGC)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
Email: [ccpds@mail.nih.gov](mailto:ccpds@mail.nih.gov)  
Tissue Procurement: NCI  
cDNA Library Preparation: Michael Brownstein Laboratory  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

**FEATURES**  
source

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Location/Qualifiers

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Site.2: SfiI (ggccgctggccc); Double-stranded cDNA was  
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cancer, breast, brain, colon, esophagus, liver, lung, muscle,  
kidney - 4%, prostate - 5.7%, lung - 10.4%, NK-cell - 5.2%,  
ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary  
gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were  
5'-AGACAGATGTCATGACAGAGTGGCATACGCGG-3' and  
5'-ATTCTAGAGCCGAGAGCGCGCAGATG-AT(30)NN-3'. Full-length  
enriched library was constructed using the Clontech  
SMART Kit and size-selected to contain the 0.2-0.5  
kb range. The library was constructed in the pBMR-1B  
library created in the laboratory of M. Brownstein (NIH).  
Note: This is a NIH MGC library." 338 a 154 c 177 g 128 t 18 others

Query Match 5.5%; Score 47.6; DB 13: Length 815;  
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Matches 86; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 715 AGACTACTTATCAGCAGACACTGCTGTCTACGACACCTTACAGCTGCTCTC 774  
DB 153 TTTTCTTCATGAGACCTGTTCTGTCATGCAATATGATGATTCGAAAAA 212  
QY 775 AATATGCTGTAACAGAAATGTTATTAACATGCTGTTCAATATGAATAAATAA 834  
DB 213 AAAATCATCATATGGAATAAATAAATAAATAAATAAATAAATAAATAA 272  
QY 835 GTTGAAATGAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 864  
DB 273 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 302

**RESULT 12**  
**LOCUS** BU589755  
**DEFINITION** AGNCOURT\_8907846 NIH\_MGC\_141 Homo sapiens cDNA clone IMAGE:638687  
**VERSION** BU589755  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

**REFERENCE**  
**AUTHORS** NIH-MGC http://mgc.ncl.nih.gov/  
**JOURNAL** National Institutes of Health, Mammalian Gene Collection (MGC)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
Email: [ccpds@mail.nih.gov](mailto:ccpds@mail.nih.gov)  
Tissue Procurement: NCI  
cDNA Library Preparation: Michael Brownstein Laboratory  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L1009851 row: i column: 08



TITLE	JOURNAL
1. The Effect of Temperature on the Rate of Reaction of Hydrogen Peroxide with Potassium Iodide	Journal of Chemical Education
2. The Effect of Concentration on the Rate of Reaction of Hydrogen Peroxide with Potassium Iodide	Journal of Chemical Education
3. The Effect of Catalyst on the Rate of Reaction of Hydrogen Peroxide with Potassium Iodide	Journal of Chemical Education
4. The Effect of Surface Area on the Rate of Reaction of Hydrogen Peroxide with Potassium Iodide	Journal of Chemical Education
5. The Effect of pH on the Rate of Reaction of Hydrogen Peroxide with Potassium Iodide	Journal of Chemical Education
6. The Effect of Pressure on the Rate of Reaction of Hydrogen Peroxide with Potassium Iodide	Journal of Chemical Education
7. The Effect of Solvent on the Rate of Reaction of Hydrogen Peroxide with Potassium Iodide	Journal of Chemical Education
8. The Effect of Light on the Rate of Reaction of Hydrogen Peroxide with Potassium Iodide	Journal of Chemical Education
9. The Effect of Time on the Rate of Reaction of Hydrogen Peroxide with Potassium Iodide	Journal of Chemical Education
10. The Effect of Temperature on the Rate of Reaction of Hydrogen Peroxide with Potassium Iodide	Journal of Chemical Education